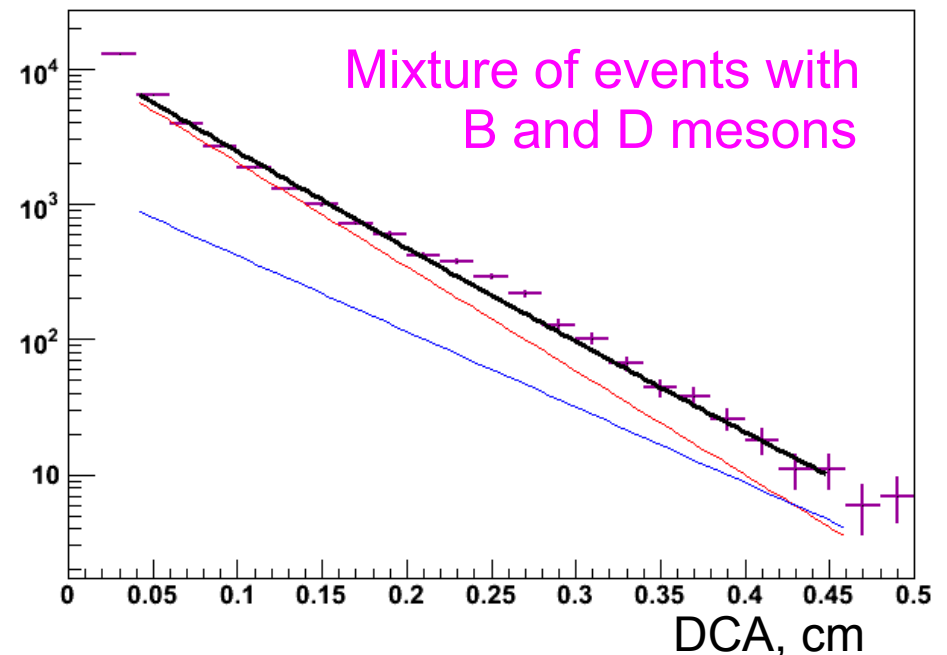
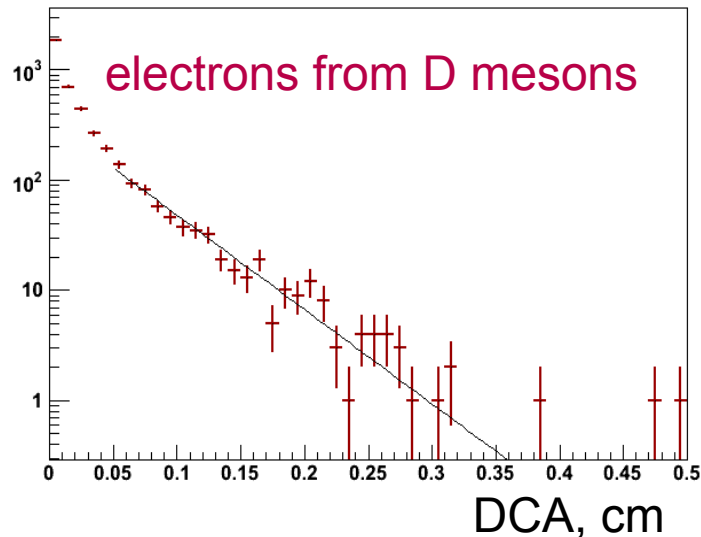
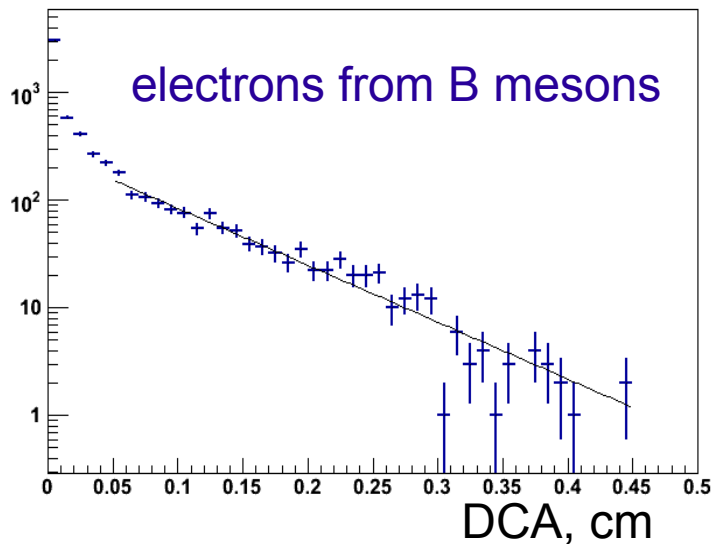


# Update on Charm/Bottom Separation

*Sasha Lebedev, ISU*

# Reminder

- Embed electrons from B and D meson decays in p+p PYTHIA events
- Run full simulation and reconstruction, DCA from Kalman Fit.
  - Fit DCA distributions for charm and bottom separately with an exponential for each  $p_T$  bin, obtain slopes.
  - Mix events with charm and bottom, fit DCA distribution for the mixture with two exponentials with the slopes from previous step (for each  $p_T$  bin).



# What is new?

The problem with this approach is that you need to know what is DCA slope for B mesons and for D mesons separately, before you attempt the separation.

If we try to predict the slopes from a separate simulation of B and D mesons, we need to know  $p_T$  distribution for B and D mesons.

If you use wrong  $p_T$  distribution, this procedure does not work.

New approach: predict DCA slopes for B and D from a measurement.

DCA slopes can be predicted from one measurement of DCA slope for the charm/bottom mixture at low  $p_T$  (where it is close to DCA slope for charm).

This works for different data sets with different  $p_T$  distributions.

No need to know in advance DCA slopes for B and D mesons, they can be predicted from a measurement!

# The Procedure

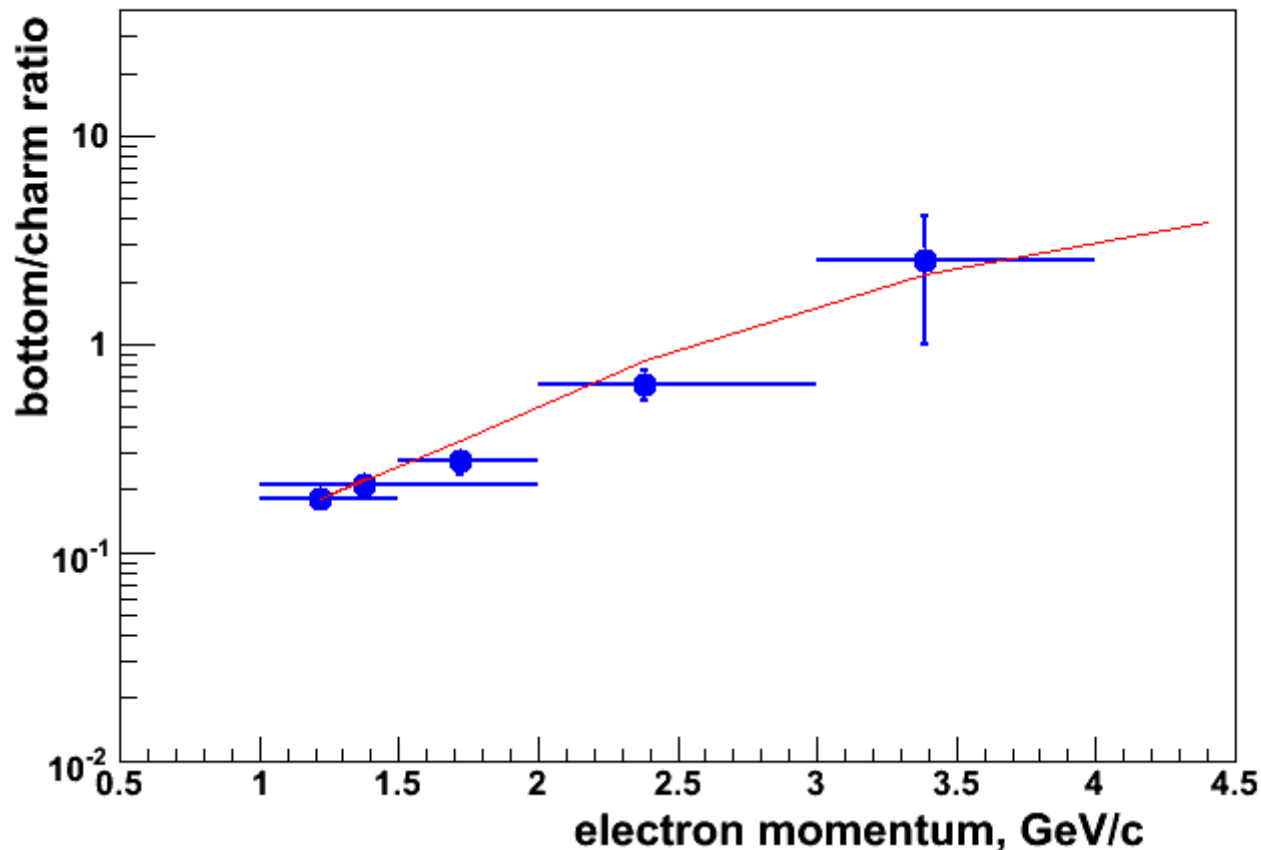
- Measure DCA slope in 1-2 GeV  $p_T$  bin for the charm+bottom mixture, call it  $S_O$ .
  - From this number, for a given  $p_T$  bin, calculate DCA slopes for charm and bottom like this:
$$S_{\text{CHARM}} = 1.1 S_O \text{ pow}(p_T, 0.1)$$
$$S_{\text{BOTTOM}} = 1.1 S_O \text{ pow}(p_T, 0.1) / 1.5$$
  - In a given  $p_T$  bin, fit DCA distribution for the B+D mixture by:
$$[0] * \exp(-\text{DCA} * S_{\text{CHARM}}) + [1] * \exp(-\text{DCA} * S_{\text{BOTTOM}})$$
  - Ratio of fit parameters [1] and [0] is bottom/charm ratio in this  $p_T$  bin.
- Examples of separation are shown in the following slides.

# Example of Separation (Dataset 1)

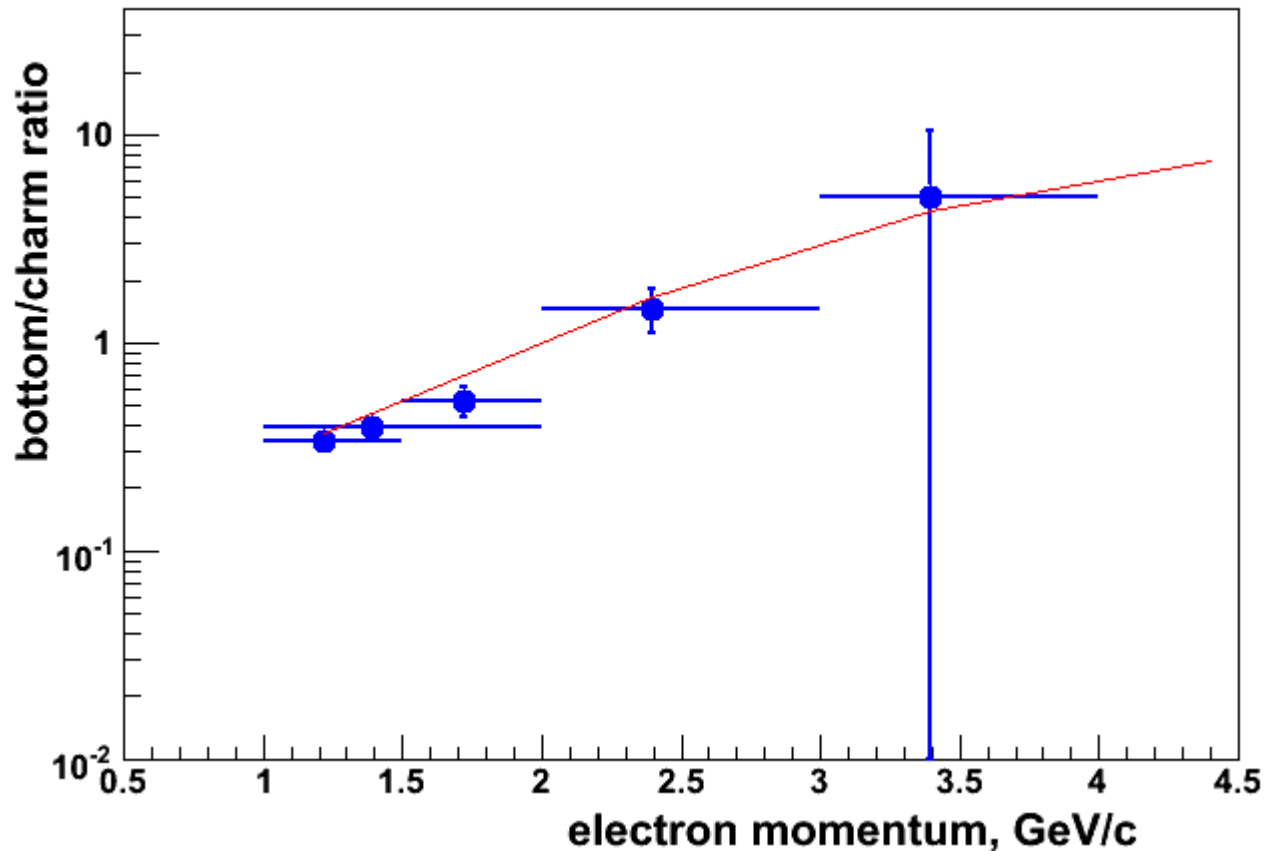
Red – true bottom/charm ratio

Blue – reconstructed bottom/charm ratio

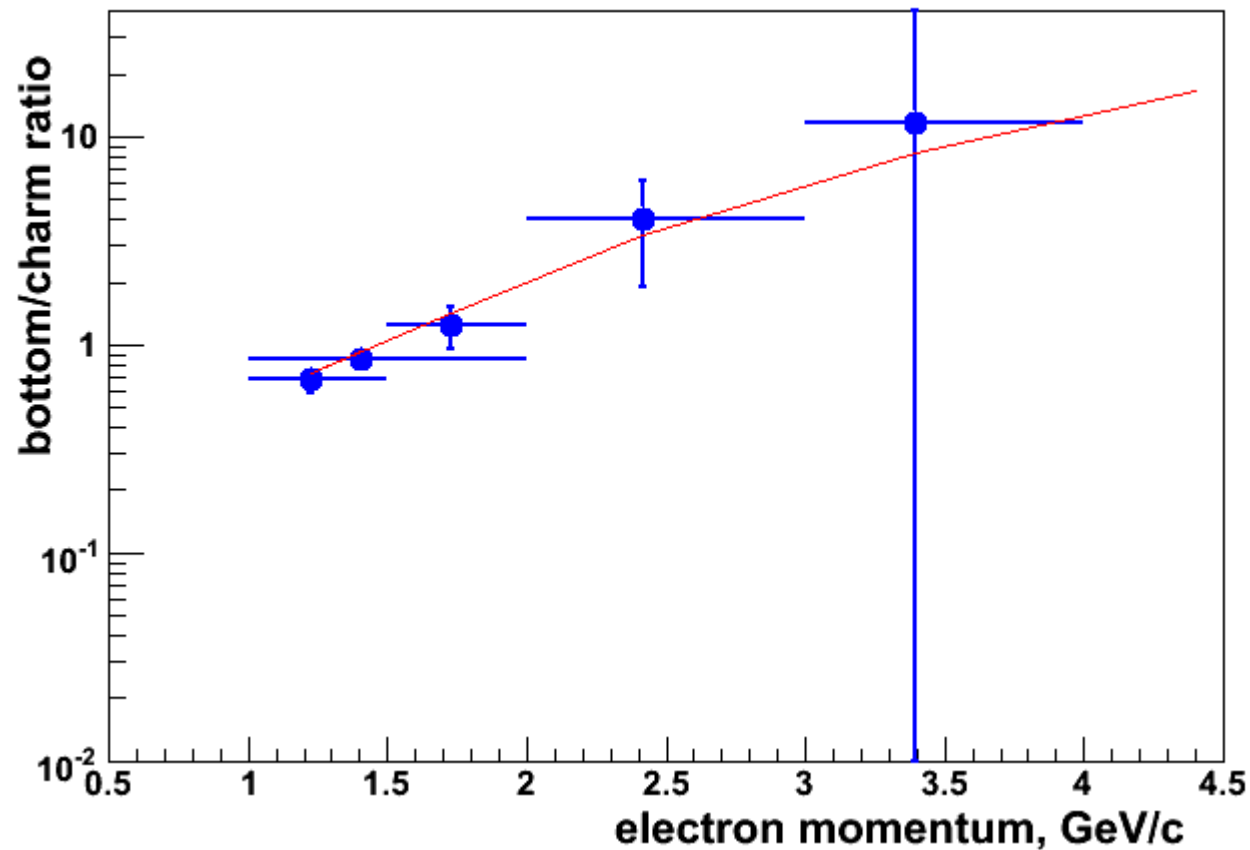
*Horizontal error bars indicate bin width, vertical error bars fit errors*



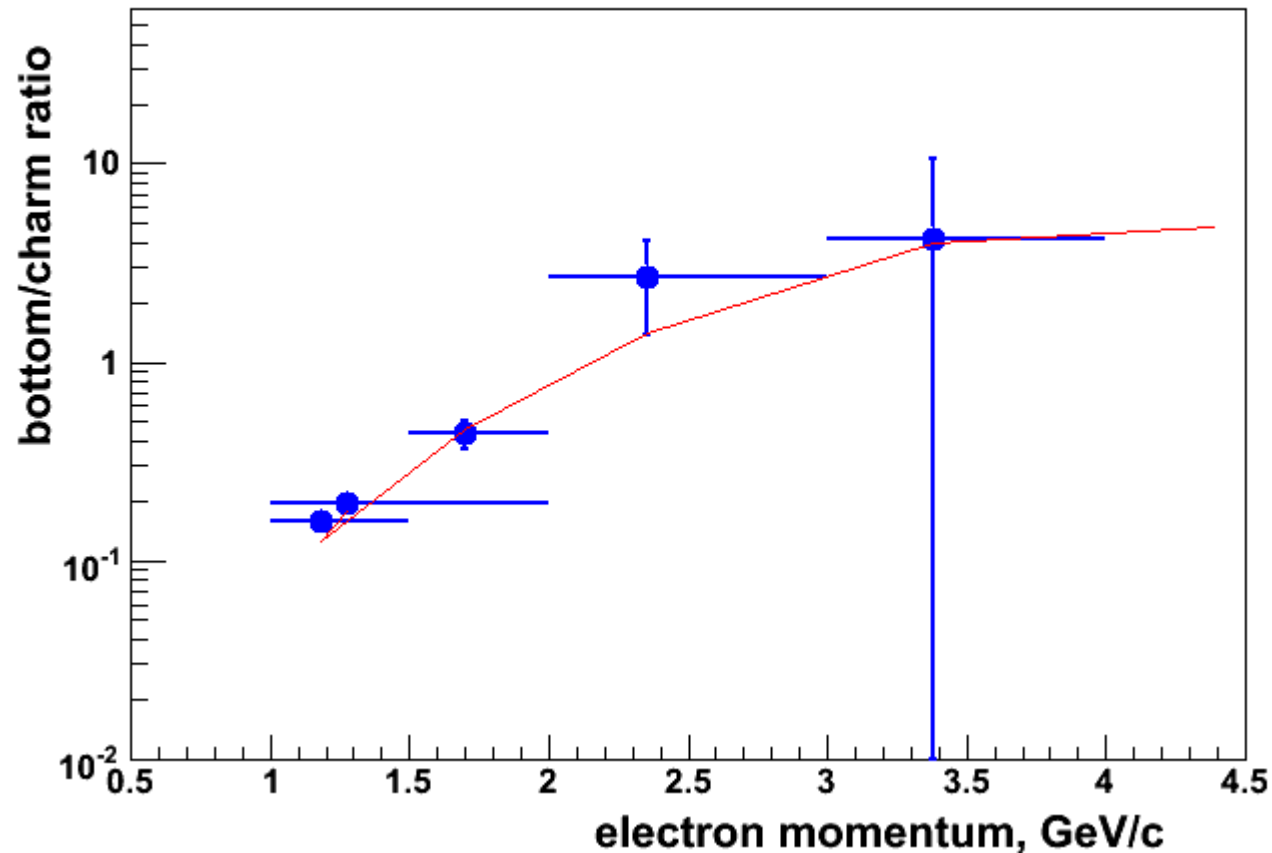
# Example of Separation (Dataset 1)



# Example of Separation (Dataset 1)



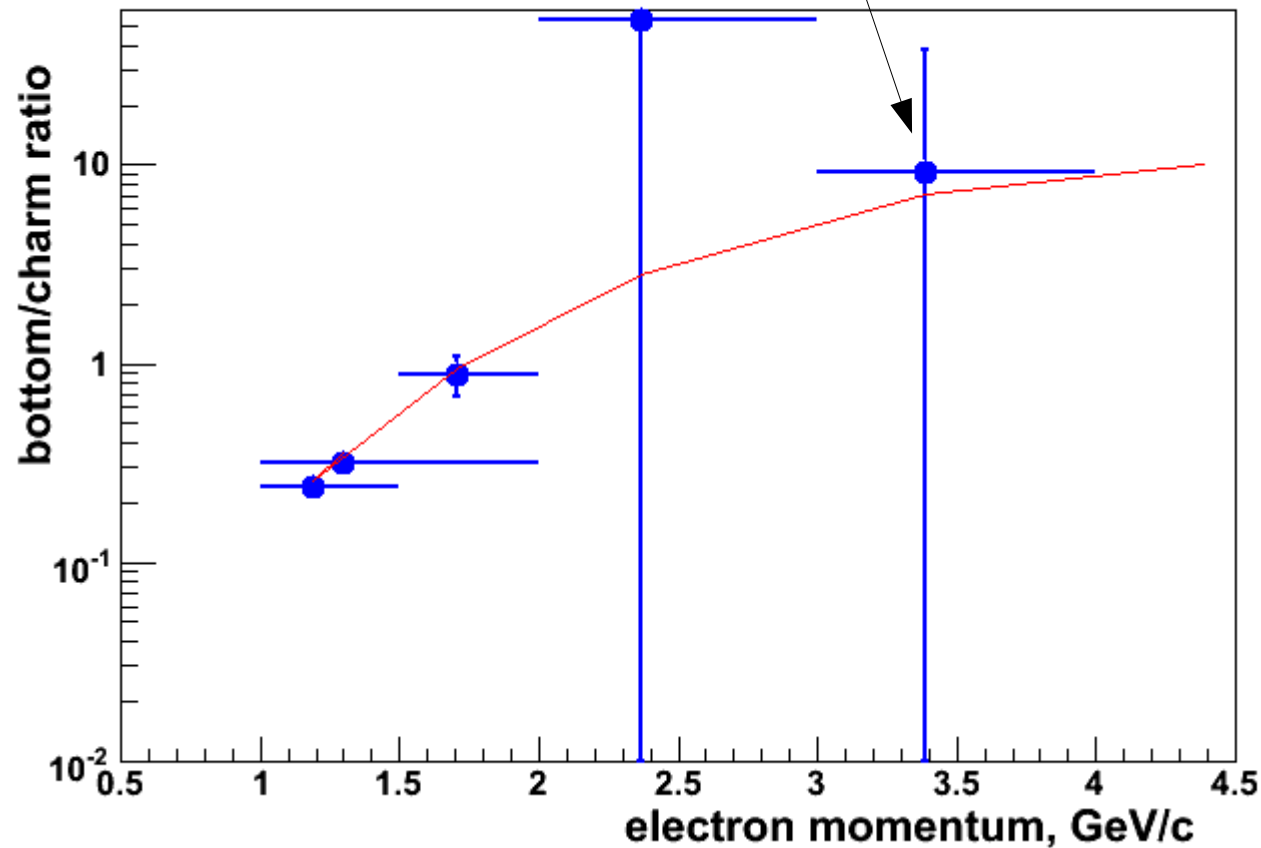
# Example of Separation (Dataset 2)





# Example of Separation (Dataset 2)

The procedure requires good statistics.  
Without it, fitting does not work.



# Summary and Plans

- The procedure seems to work well for two data sets (min. bias and  $\text{ckin}(3)=3\text{GeV}$ ).
- Should try it for some other datasets, also would be good if someone else tried to use it.
- Blind analysis?

The code for this analysis is in cvs:

*offline/analysis/run7\_jpsi\_isu/AnaAnalysis.cc*

*offline/analysis/run7\_jpsi\_isu/work/plot/plotbdsepnew.C*

I will create documentation at VTX Wiki page:

*[https://www.phenix.bnl.gov/WWW/offline/wikioffline/index.php/VTX\\_%28SVX%29](https://www.phenix.bnl.gov/WWW/offline/wikioffline/index.php/VTX_%28SVX%29)*